

Characterization of a Novel Composite Staphylococcal Cassette Chromosome *mec* in Methicillin-Resistant *Staphylococcus pseudintermedius* from Thailand

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A novel staphylococcal cassette chromosome *mec* (SCC*mec*) composite island (SCC*mec*_{AI16}-SCC*czzr*_{AI16}-CI) was identified in *Staphylococcus pseudintermedius*. Four integration site sequences for SCC subdivided the 60,734-bp island into 41,232-bp SCC*mec*_{AI16}, 19,400-bp SCC*czzr*_{AI16}, and 102-bp SCC-like_{AI16} elements. SCC*mec*_{AI16} represents a new combination of *ccrA1B3* genes with a class A *mec* complex. SCC*czzr*_{AI16} contains *ccrA1B6* and genes related to restriction modification and heavy metal resistance. SCC*mec*_{AI16}-SCC*czzr*_{AI16}-CI was found in methicillin-resistant *S. pseudintermedius* sequence type 112 (ST112) and ST111 isolated from dogs and veterinarians in Thailand.

Methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) has been associated with clinical manifestations in companion animals and occasionally causes diseases in humans (1, 2). MRSP contains the staphylococcal cassette chromosome *mec* (SCC*mec*) element, which is defined by the presence of the *mec* gene that mediates β -lactam resistance and by the cassette chromosome recombinase (*ccr*) gene(s) responsible for site-specific integration/excision of the element (3). Composite SCC structures containing two *ccr* gene complexes likely resulting from multiple element integrations have been increasingly reported in *Staphylococcus aureus* and in coagulase-negative staphylococci where such structures frequently carry heavy metal resistance gene clusters (3–9). So far, only five SCC*mec* elements have been completely characterized in MRSP, including SCC*mec* II–III, SCC*mec* VII–241, SCC*mec* V, Ψ SCC*mec*₅₇₃₉₅, and SCC*mec* IV, and are mainly associated with predominant clones of the following sequence types (ST): ST71, ST93, ST68, ST233, ST45, and ST261 (10–14). Recently, MRSP strains of ST112 and ST111 (a single locus variant of ST112) isolated from dogs and veterinarians in Thailand were found to contain an unusual combination of the class A *mec* gene complex with the type I *ccr* gene complex, suggesting a new SCC*mec* type (15). We therefore aimed to characterize this novel SCC*mec* element and to determine whether it is conserved within other MRSP isolates of the same clonal lineage.

Identification of the SCC*mec*_{AI16}-SCC*czzr*_{AI16} composite element (CI). MRSP strains of ST111 and ST112 were obtained from a previous study and are listed in Table 1 (15). Phenotypic and genotypic characteristics, including those determined by antimicrobial susceptibility testing and antibiotic resistance gene detection, pulsed-field gel electrophoresis (PFGE), and multilocus sequence typing (MLST), were determined previously (15). In this study, the strains were additionally tested for *mec*-associated direct repeat unit (*dru*) and *spa* types (16, 17), for the presence of the novel SCC*mec* element, and for resistance to heavy metals. The genomic DNA of all strains was extracted using the peqGOLD bacterial DNA kit (Peqlab Biotechnologie GmbH, Jena, Germany), and that of strain AI16 was sequenced using Ion Torrent semiconductor (Life Technologies, Carlsbad, CA) and Illumina MiSeq (Illumina, San Diego, CA) technologies. Sequence reads

from the Ion Torrent were assembled *de novo* using MIRA v3.4.1.1, generating 64 contigs with an N_{50} (length weighted median) of 121,469 bp and a contig sum of 2,829,899 bp (mean read length, 265 bp; average coverage, >100-fold). The sequences were corrected by read mapping with MiSeq reads using Geneious version R8 (Biomatters, Auckland, New Zealand) (18), and unresolved discrepancies were verified by Sanger sequencing (ABI Prism 3100 genetic analyzer; Applied Biosystems, Foster City, CA). Nucleotide analysis searching for SCC-associated components (*orfX* gene, *mec* gene complexes, *ccr* gene complexes, and integration site sequence [ISS] for SCC [19]) using BLAST (<http://blast.ncbi.nlm.nih.gov/>) enabled the identification of a 60,734-bp SCC composite element within a 100,011-bp contig. Open reading frames (ORF) were defined using Prodigal software for locating genes in prokaryotes (34) and were annotated manually using BLASTn and BLASTp algorithms. The element was integrated at the 3' end of the chromosomal *orfX* gene and contained a *mec* gene complex, two *ccr* gene complexes, and four ISSs. The ISSs contained direct repeats (DRs) that flanked the composite SCC element and that also divided it into three subunits, including SCC*mec*_{AI16}, SCC*czzr*_{AI16}, and SCC-like_{AI16} according to the International Working Group on the Classification of Staphylococcal Cassette Chromosome Elements (IWG-SCC) (4) (Fig. 1). ISSs were also linked to imperfect inverted repeats (IRs) at all

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TABLE 1 Origin and molecular characteristics of the six methicillin-resistant *Staphylococcus pseudintermedius* strains used in this study

Strain	Source	Site	Sequence type ^a	PFGE result ^a	SCCmec ^b	spa type ^c	dru type ^d	Antimicrobial resistance profile [resistance genes] ^e
AI16	Dog	Groin with crusty exudate	ST112	A	SCCmec _{AI16} -SCCczr _{AI16} -CI	t05	11y	OXA-PEN-TET-GEN-KAN-STR-ERY-iCLI-SMX-TMP [<i>mecA</i> , <i>blaZ</i> , <i>tet</i> (M), <i>aac</i> (6')-Ie, <i>ant</i> (6')-Ia, <i>aph</i> (2')-Ia, <i>aph</i> (3')-III, <i>erm</i> (B), <i>sat4</i> and <i>dfrG</i>]
AJ1	Dog	Perineal carriage	ST112	A	SCCmec _{AI16} -SCCczr _{AI16} -CI with 1,868-bp insertion	t05	11cv	OXA-PEN-TET-GEN-KAN-STR-ERY-CLI-SMX-TMP-MUP [<i>mecA</i> , <i>blaZ</i> , <i>tet</i> (K), <i>tet</i> (M), <i>aac</i> (6')-Ie, <i>ant</i> (6')-Ia, <i>aph</i> (2')-Ia, <i>aph</i> (3')-III, <i>erm</i> (A), <i>erm</i> (B), <i>sat4</i> , <i>dfrG</i> and <i>mupA</i>]
AK5	Dog	Nasal carriage	ST112	A	SCCmec _{AI16} -SCCczr _{AI16} -CI	t05	11y	OXA-PEN-TET-GEN-KAN-STR-ERY-iCLI-SMX-TMP [<i>mecA</i> , <i>blaZ</i> , <i>tet</i> (K), <i>tet</i> (M), <i>aac</i> (6')-Ie, <i>ant</i> (6')-Ia, <i>aph</i> (2')-Ia, <i>aph</i> (3')-III, <i>erm</i> (B), <i>sat4</i> and <i>dfrG</i>]
AM33	Dog	Perineal carriage	ST111	C	SCCmec _{AI16} -SCCczr _{AI16} -CI	Negative	11y	OXA-PEN-TET-GEN-KAN-STR-ERY-iCLI-SMX-TMP [<i>mecA</i> , <i>blaZ</i> , <i>tet</i> (K), <i>aac</i> (6')-Ie, <i>ant</i> (6')-Ia, <i>aph</i> (2')-Ia, <i>aph</i> (3')-III, <i>erm</i> (B), <i>sat4</i> and <i>dfrG</i>]
VA26	Human	Nasal carriage	ST112	A	SCCmec _{AI16} -SCCczr _{AI16} -CI with 1,868-bp insertion	t06	11y	OXA-PEN-TET-GEN-KAN-STR-ERY-iCLI-SMX-TMP-CIP [<i>mecA</i> , <i>blaZ</i> , <i>tet</i> (M), <i>aac</i> (6')-Ie, <i>ant</i> (6')-Ia, <i>aph</i> (2')-Ia, <i>aph</i> (3')-III, <i>erm</i> (B), <i>sat4</i> and <i>dfrG</i>]
VB16	Human	Nasal carriage	ST112	A	SCCmec _{AI16} -SCCczr _{AI16} -CI	t06	11y	OXA-PEN-TET-GEN-KAN-STR-ERY-CLI-SMX-TMP-MUP-CIP [<i>mecA</i> , <i>blaZ</i> , <i>tet</i> (M), <i>aac</i> (6')-Ie, <i>ant</i> (6')-Ia, <i>aph</i> (2')-Ia, <i>aph</i> (3')-III, <i>erm</i> (B), <i>sat4</i> , <i>dfrG</i> and <i>mupA</i>]

^a MLST and PFGE analyses were performed as a part of the previous study (15).

^b SCCmec_{AI16}-SCCczr_{AI16}-CI was identified in all strains by long-range PCR and restriction analysis. AJ1 and VA26 contained a 1,868-bp insertion.

^c The *spa* typing resulted in two *spa* types, t05 (r01-r02-r03-r03-r03-r06-r05) and t06 (r01-r02-r03-r03-r06-r05), and one negative strain with no *spa* amplification by PCR.

^d The *dru* types presented *dru* repeats as follows: 11y, 5a-2d-4a-1b-2d-5b-3a-2g-3b-4e-3e; 11cv, 5a-2d-4a-1b-2d-6f-3a-2g-3b-4e-3e.

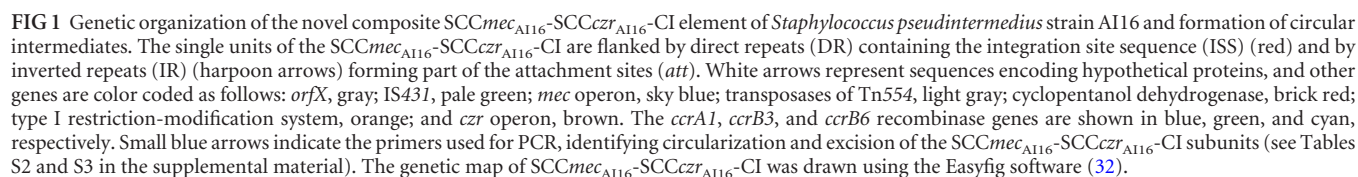
^e Antimicrobial resistance phenotypes and detection of resistance genes were determined in the previous study using broth dilution methods and microarray (15). Abbreviation of antimicrobials are as follows: OXA, oxacillin; PEN, penicillin; TET, tetracycline; GEN, gentamicin; KAN, kanamycin; STR, streptomycin; ERY, erythromycin; CLI, clindamycin; iCLI, inducible resistance to clindamycin; SMX, sulfamethoxazole; TMP, trimethoprim; MUP, mupirocin; CIP, ciprofloxacin. Antibiotic resistance genes and functions are as follows: *mecA*, penicillin-binding protein 2a; *blaZ*, β-lactamase; *tet*(K), tetracycline efflux protein; *tet*(M), ribosomal protective protein; *aac*(6')-Ie, aminoglycoside acetyltransferase; *ant*(6')-Ia, aminoglycoside nucleotidyltransferase; *aph*(2')-Ia and *aph*(3')-III, aminoglycoside phosphotransferases; *erm*(B) and *erm*(C), erythromycin resistance methylase; *sat4*, streptothricin acetyltransferase; *dfrG*, dihydrofolate reductase; *mupA*, isoleucyl-tRNA synthetase.

subunit boundaries, forming parts of the SCC attachment sites (*att*) (19) (Fig. 1).

SCCmec_{AI16}. SCCmec_{AI16} consisted of a classical SCCmec element, as it contained the *mec* gene as well as the *ccr* genes and was flanked by two DRs (DR1 and DR2). It was located downstream of *orfX*, had a size of 41,232 bp, and contained 44 ORFs. The class A *mec* gene complex was located directly downstream of *orfX* and was only separated by a small 108-bp noncoding joining region (Fig. 1). The second joining region of SCCmec_{AI16} spanning the region between the *mec* gene complex and the *ccr* gene complex contained several genes coding for hypothetical protein, cadmium resistance (*cadCAD*), transposase B and C of transposon Tn554, and a putative cyclopentanol dehydrogenase (*cpnA*). The entire 5' region of SCCmec_{AI16}, including the *mec* gene complex up to *cpnA*, was highly identical (99%) to the nucleotide sequence of SCCmec VII-241 (without *cpnA*) and to a hybrid SCCmec-*mecC* region of *Staphylococcus sciuri* GVG52 (including *cpnA*) (10, 21). However, SCCmec_{AI16} differed from those two elements by the presence of a different type of *ccr* gene complex and a different 3' end-joining region that encoded various hypothetical proteins, some of them already identified in other SCCmec elements (see Table S1 in the supplemental material). The *ccr* complex of SCCmec_{AI16} contained *ccrA1* and *ccrB3* genes and shared the closest identity to those of *S. aureus* JCSC6945 and *S. sciuri* MCS24 with 92% and

89% nucleotide identity, respectively (20, 22) (see Fig. S1 in the supplemental material). *ccrA1B3* was assigned as a type 8 *ccr* complex, which was originally found in SCCmec XI together with a class E *mec* complex in *S. aureus* M10/0061 (23). However, the *ccrA1* of SCCmec_{AI16} shared only 81% nucleotide identity with the *ccrA1* of SCCmec XI but shared up to 90% sequence similarity with the *ccrA1* in SCCmec IX and X in livestock-associated methicillin-resistant *S. aureus* (LA-MRSA) in Thailand (20, 24). The combination of the type 8 *ccr* complex and the class A *mec* complex of SCCmec_{AI16} has not been previously reported and represents a new SCCmec type in *S. pseudintermedius*.

SCCczr_{AI16} and SCC-like_{AI16}. The SCCczr_{AI16} element contained recombinase genes but no *mec* gene. It was flanked by DR2 and DR3, arranged in tandem with the SCCmec_{AI16}, and followed by a 102-bp noncoding SCC-like_{AI16} fragment demarcated by DR3 and DR4. SCCczr_{AI16} was 19 kb in length, contained 18 ORFs (see Table S1 in the supplemental material), and consisted of three main segments displaying different functions. The first segment contained genes coding for proteins (HsdR, HsdM, and HsdS) associated with a type I restriction-modification system. HsdR and HsdM showed 99% and 98% amino acid (aa) identity with those encoded on SCCfusC, respectively (25), and were combined with a novel HsdS that shared 61% aa identity to the closest HsdS (see Table S1), indicating a new restriction specificity in this



Presence of SCCmec_{AI16}-SCCczr_{AI16}-CI in additional MRSP isolates. Long-range PCR amplification followed by restriction analysis (see Tables S2 and S4 in the supplemental material) confirmed the overall structure of SCCmec_{AI16}-SCCczr_{AI16}-CI in MRSP strain AI16 and allowed detection of similar composite elements in five additional clonally related MRSP strains of ST111 and ST112 isolated from dogs and humans (Table 1). Two strains, AJ1 (ST112) and VA26 (ST112), showed a minor variation in the restriction analysis caused by a 1,868-bp insertion between *czrC*

TABLE 2 Heavy metal susceptibility of *Staphylococcus aureus* and *Staphylococcus pseudintermedius* strains as determined using broth microdilution test

Strain	Metal resistance gene(s)	MIC (mM) of metal						Source
		CuSO ₄	CdCl ₂	ZnSO ₄	AsNaO ₂	Pb(CH ₃ COO) ₂	HgCl ₂	
<i>S. aureus</i> RN4220		4	≤0.015	0.5	0.03	≤0.125	≤0.015	33
<i>S. pseudintermedius</i> CCUG 49543 (=LMG 22219)		16	0.25	1	2	1	≤0.015	Culture Collection, University of Göteborg, Sweden
Methicillin-resistant <i>S. pseudintermedius</i> E120		16	0.25	1	2	1	≤0.015	1
KM241	<i>cadA</i>	16	1	1	2	1	≤0.015	10
196511	<i>czcC</i>	16	0.25	1	2	1	≤0.015	D. Elad, Kimron Veterinary Institute, Bet Dagan, Israel
AI16	<i>cadA</i> , <i>czcC</i>	16	1	1	2	1	≤0.015	This study, 15

and ISS3 as confirmed by primer walking and Sanger sequencing. In addition, the *SCCmec* element of AJ1 displayed an alternative hypervariable repeat region (*dru* 11cv) that was different from that of the other strains (*dru* 11y), suggesting different evolution-ary processes within SCC of the same clonal lineage.

Characterization of the novel *SCCmec*_{AI16}-*SCCczr*_{AI16}-CI element in *S. pseudintermedius* revealed regions with homology to other *SCCmec* elements. The 5' region of *SCCmec*_{AI16} obviously shared a common ancestral origin with *SCCmec* elements found in *S. pseudintermedius* KM241 and in *S. sciuri* GVGS2 but displayed a substituted 3' region resulting in a new combination of the class A *mec* complex with *ccrA1B3* genes. The presence of *SCCczr*_{AI16} harboring a second *ccrAB* complex illustrates the challenge for PCR-based *SCCmec* typing. Furthermore, the location of two related *ccrAB* gene complexes aligned in proximity offer a source for homologous recombination-mediated deletion, a mechanism observed previously with *ccrC* sequences (28, 31). The presence of this composite element in other strains of the same lineage rather supported a spread of this cassette with a clone as opposed to an autonomous transfer between strains. However, the ability of the *SCCmec*_{AI16}-*SCCczr*_{AI16}-CI subunits to circularize independently may play a role in the mobilization and in the further evolutionary diversification of this composite *SCCmec* structure.

Nucleotide sequence accession numbers. The nucleotide sequences of the *SCCmec*_{AI16}-*SCCczr*_{AI16}-CI of *S. pseudintermedius* AI16 and the 1,868-bp insertion in *S. pseudintermedius* VA26 have been deposited in GenBank under accession numbers LN864705 and LN874217, respectively.

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